

SEQUENCE LISTING

<110> Jackson, W. James
 Pace, John
 <120> Chlamydia Protein, Gene Sequence and Uses Thereof
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 <140> 09/612,402
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 <150> 08/942,596
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 ctgagccaag caaaggatag agaaagtcttg taatcatcgc aggttaaagg gggatgtta 240
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 aagataagaa catttatttga tattaaatta ttaattttttt atgaagcggaa gtaattaaattt 360
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 act gta tca ttt ccc tat act gtt ata gga gat ccg agt ggg act act 555
 Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr
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 gca gct ttg cct tta agt tgt ttt ggg aac tta tta ggg agt ttt act 651
 Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr
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 Val Leu Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser
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Ile Glu Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu	
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gcc gta ctg cct gct gca acg act aat aag ggt agc cag act ccg acg	843
Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr	
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Thr Thr Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu	
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175 180 185	
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Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr	
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Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu	
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Val Ser Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr	
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460 465 470	
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495 500 505	
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Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val	
510 515 520	
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cat gaa tct ttt aca gag gaa ggc gat caa gct cgg gca ttc aag agc	3099
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Gly His Leu Leu Asn Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg	
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Cys Ser Ser Thr His Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile	
925 930 935	
tgt gat gct tat cgc acc atc tct ggt act gag aca acg ctc cta tcc	3243
Cys Asp Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser	
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cat caa gag aca tgg aca aca gat gcc ttt cat tta gca aga cat gga	3291
His Gin Glu Thr Trp Thr Thr Asp Ala Phe His Leu Ala Arg His Gly	
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Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu	
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Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His	
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Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr	
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260 265 270	
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 Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys Arg Thr Ala Lys
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 Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln Ala Ile
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 Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys Ala Lys
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 Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr Thr Leu
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 Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His Asp Arg
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Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His Leu Leu Asn Leu
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Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His Pro
915 920 925
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945 950 955 960
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attgctgctg	ttcaggatgg	gcagcaggg	gtgtcatcat	ctacttcaac	agaagatcca	720
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ggagggattt	actcctacgg	gaacgttgc	ttccTgataa	atggaaaaac	cttggTTCTC	840
aacaatgtt	tttccctgt	ttacattgc	gctaagcaac	caacaagtgg	acaggcttct	900
aatacgagta	ataattacgg	agatggagga	gctatTTCT	gtaagaatgg	tgcccaagca	960
ggatccaata	actctggatc	agtttccTT	gatggagagg	gagtagttt	ctttagtagc	1020
aatgttagctg	ctggaaagg	gggagctatt	tatgccaAAA	agctctcggt	tgctaactgt	1080
ggccctgtac	aatttttaag	gaatatcgt	aatgatggtg	gagcgttta	tttaggagaa	1140
tctggagagc	tcagTTTATC	tgctgattat	ggagatatta	tttgcgtgg	gaatcttaaa	1200
agaacagcca	aagagaatgc	tgccgatgtt	aatggcgtaa	ctgtgtcctc	acaagccatt	1260
tcgatggat	cgggagggaa	aataacgaca	ttaagagct	aagcaggca	tcaGATTCTC	1320
tttaatgatc	ccatcgagat	ggcaaacgga	aataaccagc	cagcgcagtc	ttccaaactt	1380
ctaaaaatta	acgatggtga	aggatacaca	ggggatattt	ttttgcataa	tggaaagcagt	1440
actttgtacc	aaaatgttac	gatagagcaa	ggaaggattt	ttttgcgtga	aaaggcaaaa	1500
ttatcgtga	a					1511

<210> 11
 <211> 1444
 <212> DNA
 <213> Chlamydia sp.

<400> 11

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gcatttgc	ctttcttctt	tgTTtagcaa	caatgcagtt	acgaatcctc	ctaccaatcc	180
tccagcgc	gattctcatc	ctgcagtcat	tggttagcaca	actgctgggt	ctgttacaat	240
tagtggcct	atctttttt	aggatttgg	tgatacagct	tatgataaggt	atgattggct	300
aggTTctaat	caaaaaatca	atgtcctgaa	attacagtt	gggactaagc	ccccagctaa	360
tgcTTccatca	gatttgactc	tagggatgt	gatgcctaag	tatggctatc	aaggaagctg	420
gaagcttgc	tgggatccta	atacagcaa	taatggcct	tatactctga	aagctacatg	480
gactaaaact	gggtataatc	ctgggcctga	gcgagtagct	tcttgggtc	caaatagttt	540
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gcgcTTTtat	tgtcgaggat	tatggTTTC	tggagttcg	aatttcttct	atcatgaccg	660
cgatgcTTta	ggtcaggat	atcggtat	tagtgggggt	tattccttag	gagcaaactc	720
ctactttgg	tcatcgatgt	ttggTctagc	atTTaccgaa	gtatttggta	gatctaaaga	780
ttatgttagt	tgtcgTTcca	atcatcatgc	ttgcatacgaa	tccgTTtatc	tatctaccca	840
acaagcttta	tgtggatcct	atTTgttccg	agatgcgtt	atccgtgcta	gctacgggtt	900
tggaaatcag	catataaaa	cctcatatac	atTTgcagag	gagagcgtat	tgcTTggga	960
taataactgt	ctggctggag	agattggagc	gggattaccg	attgtgatta	ctccatctaa	1020
gctctattt	aatgagtTgc	gtcTTTcgt	gcaagctgag	ttttctttagt	ccgatcatga	1080
atcttttaca	gaggaaggcg	atcaagctcg	ggcattcaag	agcggacatc	tccTaaatct	1140
atcagTTcc	gttggagtga	agTTgtatcg	atgttctagt	acacatccta	ataaaatata	1200
ctttagggcg	gcttataatc	gtgtatgc	tcgcaccatc	tctggTactg	agacaacgc	1260
cctatccc	caagagacat	ggacaacaga	tgcTTTcat	ttagcaagac	atggagttgt	1320
ggttagagga	tctatgtatg	cttctcta	aagtaatata	gaagtatatg	gccatggaa	1380
atatgagtagt	cgagatgctt	ctcgaggc	tggTTgagt	gcaggaagta	gagtccgg	1440
ctaa						

<210> 12
 <211> 56
 <212> DNA
 <213> Chlamydia sp.

<400> 12
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<210> 13

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<211> 56
<212> DNA
<213> Chlamydia sp.

<400> 13
aagggcccaa ttacgcagag ggtaccctaa gaagaaggca tgccgtgcta gcggag 56

<210> 14
<211> 57
<212> DNA
<213> Chlamydia sp.

<400> 14
aagggcccaa ttacgcagag ggtaccggag agctcgcgaa tccatacgaa taggaac 57

<210> 15
<211> 1013
<212> PRT
<213> Chlamydia sp.

<400> 15
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1 5 10 15
Ser Cys Cys Ser Leu Asn Gly Gly Tyr Ala Ala Glu Ile Met Val
20 25 30
Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr
35 40 45
Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu
50 55 60
Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser
65 70 75 80
Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His
85 90 95
Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu
100 105 110
Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu
115 120 125
Leu Ser Phe Ser Asn Cys Asn Pro Leu Leu Ala Val Leu Pro Ala Ala
130 135 140
Thr Thr Asn Asn Gly Ser Gln Thr Pro Ser Thr Thr Ser Thr Pro Ser
145 150 155 160
Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn Asn Glu
165 170 175
Lys Phe Ser Phe Tyr Ser Asn Ser Val Ser Gly Asp Gly Gly Ala Ile
180 185 190
Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe
195 200 205
Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr
210 215 220
Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val Ala Asn
225 230 235 240
Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp Gly Gln
245 250 255
Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val Ser Phe
260 265 270
Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg Val Gly
275 280 285
Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys
290 295 300
Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala Ala Glu
305 310 315 320

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Gln Pro Thr Asn Gly Gln Ala Ser Asn Thr Ser Asp Asn Tyr Gly Asp
 325 330 335
 Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Ala Gly Ser Asn
 340 345 350
 Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe Ser
 355 360 365
 Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala Lys Lys Leu
 370 375 380
 Ser Val Ala Asn Cys Gly Pro Val Gln Leu Leu Gly Asn Ile Ala Asn
 385 390 395 400
 Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu Ser
 405 410 415
 Ala Asp Tyr Gly Asp Met Ile Phe Asp Gly Asn Leu Lys Arg Thr Ala
 420 425 430
 Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln Ala
 435 440 445
 Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys Ala
 450 455 460
 Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly Asn
 465 470 475 480
 Asn Gln Pro Ala Gln Ser Ser Glu Pro Leu Lys Ile Asn Asp Gly Glu
 485 490 495
 Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Asn Ser Thr Leu Tyr
 500 505 510
 Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys Ala
 515 520 525
 Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Ser Leu Tyr Met
 530 535 540
 Glu Ala Gly Ser Thr Leu Asp Phe Val Thr Pro Gln Pro Pro Gln Gln
 545 550 555 560
 Pro Pro Ala Ala Asn Gln Ser Ile Thr Leu Ser Asn Leu His Leu Ser
 565 570 575
 Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr Asn
 580 585 590
 Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr Ala
 595 600 605
 Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe Glu Asp Leu Asp Asp
 610 615 620
 Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile Asp
 625 630 635 640
 Val Leu Lys Leu Gln Leu Gly Thr Gln Pro Pro Ala Asn Ala Pro Ser
 645 650 655
 Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly Ser
 660 665 670
 Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr Thr
 675 680 685
 Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg
 690 695 700
 Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile
 705 710 715 720
 Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr
 725 730 735
 Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His Asp
 740 745 750
 Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser
 755 760 765
 Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe
 770 775 780
 Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn
 785 790 795 800
 His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Lys Gln Ala Leu
 805 810 815

Cys Gly Ser Tyr Val Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly
 820 825 830
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser
 835 840 845
 Asp Val Cys Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly
 850 855 860
 Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg
 865 870 875 880
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr
 885 890 895
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn
 900 905 910
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His
 915 920 925
 Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg
 930 935 940
 Thr Ile Ser Gly Thr Gln Thr Thr Leu Leu Ser His Gln Glu Thr Trp
 945 950 955 960
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly
 965 970 975
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly
 980 985 990
 Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly
 995 1000 1005
 Ser Lys Val Arg Phe
 1010

<210> 16
 <211> 1013
 <212> PRT
 <213> Chlamydia sp.

<400> 16
 Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr
 1 5 10 15
 Ser Cys Cys Ser Leu Thr Gly Gly Tyr Ala Ala Glu Ile Met Val
 20 25 30
 Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr
 35 40 45
 Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu
 50 55 60
 Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser
 65 70 75 80
 Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His
 85 90 95
 Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu
 100 105 110
 Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu
 115 120 125
 Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro Ala Ala
 130 135 140
 Thr Thr Asn Asn Gly Ser Gln Thr Pro Thr Thr Ser Thr Pro Ser
 145 150 155 160
 Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn Asn Glu
 165 170 175
 Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly Thr Ile
 180 185 190
 Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe
 195 200 205
 Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr
 210 215 220

Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Ile Ala Asn
 225 230 235 240
 Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp Gly Gln
 245 250 255
 Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val Ser Phe
 260 265 270
 Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg Val Gly
 275 280 285
 Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys
 290 295 300
 Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala Ala Glu
 305 310 315 320
 Gln Pro Thr Asn Gly Gln Ala Ser Asn Thr Ser Asp Asn Tyr Gly Asp
 325 330 335
 Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Ala Gly Ser Asn
 340 345 350
 Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe Ser
 355 360 365
 Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala Lys Lys Leu
 370 375 380
 Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Gly Asn Ile Ala Asn
 385 390 395 400
 Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu Ser
 405 410 415
 Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys Arg Thr Ala
 420 425 430
 Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln Ala
 435 440 445
 Ile Ser Met Gly Ser Gly Lys Ile Thr Thr Leu Arg Ala Lys Ala
 450 455 460
 Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly Asn
 465 470 475 480
 Asn Gln Pro Ala Gln Ser Ser Glu Pro Leu Lys Ile Asn Asp Gly Glu
 485 490 495
 Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Asn Ser Thr Leu Tyr
 500 505 510
 Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys Ala
 515 520 525
 Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser Leu Tyr Met
 530 535 540
 Glu Ala Gly Ser Thr Leu Asp Phe Val Thr Pro Gln Pro Pro Gln Gln
 545 550 555 560
 Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu Ser
 565 570 575
 Leu Ser Ser Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr Asn
 580 585 590
 Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr Ala
 595 600 605
 Gly Pro Val Thr Ile Ser Gly Pro Phe Phe Glu Asp Leu Asp Asp
 610 615 620
 Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile Asp
 625 630 635 640
 Val Leu Lys Leu Gln Leu Gly Thr Gln Pro Ser Ala Asn Ala Pro Ser
 645 650 655
 Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly Ser
 660 665 670
 Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr Thr
 675 680 685
 Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg
 690 695 700
 Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile
 705 710 715 720

Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr
 725 730 735
 Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Ser Tyr His Asp
 740 745 750
 Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser
 755 760 765
 Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe
 770 775 780
 Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn
 785 790 795 800
 His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Lys Gln Ala Leu
 805 810 815
 Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly
 820 825 830
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser
 835 840 845
 Asp Val Arg Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly
 850 855 860
 Leu Pro Ile Val Thr Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg
 865 870 875 880
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr
 885 890 895
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn
 900 905 910
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His
 915 920 925
 Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg
 930 935 940
 Thr Ile Ser Gly Thr Gln Thr Leu Leu Ser His Gln Glu Thr Trp
 945 950 955 960
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly
 965 970 975
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly
 980 985 990
 Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly
 995 1000 1005
 Ser Lys Val Arg Phe
 1010

<210> 17
 <211> 505
 <212> PRT
 <213> Chlamydia sp.

<400> 17
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 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe
 20 25 30
 Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala
 35 40 45
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu
 50 55 60
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn
 65 70 75 80
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu
 85 90 95
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val
 100 105 110
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr
 115 120 125

Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu
 130 135 140
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp
 145 150 155 160
 Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys
 165 170 175
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys
 180 185 190
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala
 195 200 205
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Ile Ala Ala Val
 210 215 220
 Gln Asp Gly Gln Gln Gly Val Ser Ser Thr Ser Thr Glu Asp Pro
 225 230 235 240
 Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val
 245 250 255
 Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu
 260 265 270
 Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr
 275 280 285
 Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn
 290 295 300
 Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala
 305 310 315 320
 Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val
 325 330 335
 Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala
 340 345 350
 Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn
 355 360 365
 Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu
 370 375 380
 Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys
 385 390 395 400
 Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser
 405 410 415
 Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg
 420 425 430
 Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala
 435 440 445
 Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn
 450 455 460
 Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser
 465 470 475 480
 Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg
 485 490 495
 Glu Lys Ala Lys Leu Ser Val Asn Ser
 500 505

<210> 18
 <211> 57
 <212> DNA
 <213> Chlamydia sp.

<400> 18
 aaggggcccaa ttacgcagag ctcgagagaa attatggttc ctcaaggaat ttacgat

57

<210> 19
 <211> 20
 <212> DNA
 <213> Chlamydia sp.

<400> 19		
cgctctagaa ctagtggatc		20
<210> 20		
<211> 22		
<212> DNA		
<213> Chlamydia sp.		
<400> 20		
atggttcctc aaggaattta cg		22
<210> 21		
<211> 19		
<212> DNA		
<213> Chlamydia sp.		
<400> 21		
ggtcccccat cagcgggag		19
<210> 22		
<211> 1515		
<212> DNA		
<213> Chlamydia sp.		
<400> 22		
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actgttatag gagatccgag tggactact gtttttctg caggagagtt aacattaaaa		120
aatcttgaca attctattgc agctttgcct ttaagttgtt ttgggaactt attaggaggt		180
tttactgttt tagggagagg acactcggtt actttcgaga acatacggac ttctacaaat		240
ggggcagctc taagtaatag cgctgctgtt ggactgttta ctattgaggg ttttaagaa		300
ttatcctttt ccaattgcaa ttcattactt gccgtactgc ctgctgcaac gactaataag		360
ggtagccaga ctccgacgac aacatctaca ccgtctaattt gtaatttagt ctctggagat		420
gatctttgt tactcaataa tgagaagttc tcattctata gtaatttagt ctctggagat		480
gggggagcta tagatgctaa gagcttaacg gttcaaggaa ttagcaagct ttgtgtcttc		540
caagaaaata ctgctcaagc tgatggggga gcttgcataag tagtcacccag tttctctgct		600
atggctaacg aggctcctat tgcctttgtt gcgaatgttgc caggagtaag agggggaggg		660
attgctgctg ttcaggatgg gcagcaggga gtgtcatcat ctacttcaac agaagatcca		720
gtagtaagtt tttccagaaaa tactgctgtt gagtttgatg ggaacgtac ccgacttagga		780
ggagggattt actcctacgg gaacgttgc ttcctgaata atggaaaaac cttgtttctc		840
aacaatgttgc ttctctgtt tacattgtc gctaagcaac caacaagtgg acaggcttct		900
aatacagatgttataattacgg agatggagga gctatcttct gtaagaatgg tgcgcaagca		960
ggatccaata actctgatc agtttccctt gatggagagg gtagtagttt ctttagtagc		1020
aatgttagctg ctggaaagg gggagctatt tatgcacaaa agctctcggt tgctaactgt		1080
ggccctgtac aatttttaag gaatatcgct aatgatggtg gagcgttta ttttaggagaa		1140
tctggagagc tcagtttac tgcgtgattt ggagatatta ttttcgtatgg gaatcttaaa		1200
agaaacagcca aagagaatgc tgccgtatgtt aatggcgtaa ctgtgtccctc acaagccatt		1260
tcgatggat cgggagggaa aataacgaca ttaagagcta aagcaggggca tcagattctc		1320
ttaatgtatccatcgatgtt ggcacaaacggaa aataaccaggc cagcgcgtc ttccaaactt		1380
ctaaaaatgttac acgtatggta aggatacaca gggatattt tttttgtatgg tggaaagcgt		1440
actttgttacc aaaaatgttac gatagagacaa ggaaggattt ttcttcgtatgg aaaggcaaaa		1500
ttatcgtatgg attct		1515
<210> 23		
<211> 3354		
<212> DNA		
<213> Artificial Sequence		
<220>		
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ttaactgtat	catttccta	tactgtata	ggagatccga	gtgggactac	tgtttttct	180
gcaggagagt	taacgtaaa	aatcttgac	aattcttattg	cagcttgc	ttaaagtgt	240
tttgggaact	tattaggag	tttactgtt	ttagggagag	gacactcg	gactttcgag	300
aacatacgg	cttctacaaa	tgagactgca	ctaagtgaca	gcgctaata	cggttattt	360
actattgagg	gttttaaaga	attatcttt	tccaaattgca	accattact	tgccgtactg	420
cctgctgcaa	cgactaataa	tgttagccag	actccgtc	caacatctac	accgtcta	480
ggtactattt	attctaaaac	agatctttt	ttactcaata	atgagaagtt	ctcattctat	540
agtaattcag	tctctggaga	tgggggagct	atagatgcta	agagcttaac	ggttcaagga	600
attagcaagc	tttgtgtctt	ccaagaaaat	actgctcaag	ctgatgggg	agcttgc	660
gtagtcacca	gttctctgc	tatggctaac	gaggctcta	ttgccttgt	agcgaatgtt	720
gcaggagtaa	gagggggagg	gattgctgt	gttcaggatg	ggcagcagg	agtgtcatca	780
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ctaacaagca	at	at	tttgc	tttgc	tttgc	3000
ggttatgg	tg	at	tttgc	tttgc	tttgc	3060
gttttagc	tg	at	tttgc	tttgc	tttgc	3120
tcctattcgt	at	gg	tttgc	tttgc	tttgc	3180
tttaagggg	ac	gtt	tttgc	tttgc	tttgc	3240
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 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant Expression Vector

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gagaacatac	ggacttctac	aatggagct	gcactaagt	acagcgctaa	tagcgggtaa	360
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aatgtacta	tttattctaa	aacagatctt	ttgttactca	ataatgagaa	gttctcattc	540
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ggaatttagca	agctttgtgt	cttccaagaa	aatactgctc	aagctgatgg	gggagcttgt	660
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<211> 65

<212> PRT

<213> Chlamydia sp.

<400> 25

Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala
1 5 10 15
Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Pro Leu
20 25 30
Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly
35 40 45
His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala
50 55 60

Leu

65

<210> 26

<211> 24

<212> PRT

<213> Chlamydia sp.

<400> 26

Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu Ser Leu Ser
1 5 10 15
Ser Leu Leu Ala Asn Asn Ala Val
20

<210> 27

<211> 8

<212> PRT

<213> Chlamydia sp.

<400> 27

Gly Tyr Thr Gly Asp Ile Val Phe
1 5

<210> 28

<211> 7

<212> PRT

<213> Chlamydia sp.

<400> 28

Tyr Gly Asp Ile Ile Phe Asp
1 5

<210> 29

<211> 63

<212> PRT

<213> Chlamydia sp.

<400> 29

Gly Tyr Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu
1 5 10 15
Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly
20 25 30
Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn
35 40 45
Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly
50 55 60

<210> 30

<211> 22

<212> PRT

<213> Chlamydia sp.

<400> 30

Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys
1 5 10 15

Ile Asn Asp Gly Glu Gly
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<210> 31

<211> 14

<212> PRT

<213> Chlamydia sp.

<400> 31

Ala Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu
1 5 10

<210> 32

<211> 10

<212> PRT

<213> Chlamydia sp.

<400> 32

Lys Leu Ser Val Asn Ser Leu Ser Gln Thr
1 5 10

<210> 33

<211> 45

<212> PRT

<213> Chlamydia sp.

<400> 33

Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile
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Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu
20 25 30

Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu
35 40 45

<210> 34

<211> 64

<212> PRT

<213> Chlamydia sp.

<400> 34

Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile
1 5 10 15

Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu
20 25 30

Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys
35 40 45

Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro
50 55 60

<210> 35

<211> 10

<212> PRT

<213> Chlamydia sp.

<400> 35

Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr
1 5 10

<210> 36

<211> 458

<212> PRT

<213> Chlamydia sp.

<400> 36

Gly Gly Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu
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Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly
20 25 30

Ile Ala Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser
 35 40 45
 Thr Glu Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe
 50 55 60
 Asp Gly Asn Val Ala Arg Val Gly Gly Ile Tyr Ser Tyr Gly Asn
 65 70 75 80
 Val Ala Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala
 85 90 95
 Ser Pro Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser
 100 105 110
 Asn Thr Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn
 115 120 125
 Gly Ala Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly
 130 135 140
 Glu Gly Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly
 145 150 155 160
 Ala Ile Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln
 165 170 175
 Phe Leu Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu
 180 185 190
 Ser Gly Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp
 195 200 205
 Gly Asn Leu Lys Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly
 210 215 220
 Val Thr Val Ser Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile
 225 230 235 240
 Thr Thr Leu Arg Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro
 245 250 255
 Ile Glu Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu
 260 265 270
 Leu Lys Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala
 275 280 285
 Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg
 290 295 300
 Ile Val Leu Arg Glu Lys Ala Lys Leu Ser Val Asn Ser Leu Ser Gln
 305 310 315 320
 Thr Gly Gly Ser Leu Tyr Met Glu Ala Gly Ser Thr Trp Asp Phe Val
 325 330 335
 Thr Pro Gln Pro Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr
 340 345 350
 Leu Ser Asn Leu His Leu Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala
 355 360 365
 Val Thr Asn Pro Pro Thr Asn Pro Pro Ala Gln Asp Ser His Pro Ala
 370 375 380
 Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile
 385 390 395 400
 Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu
 405 410 415
 Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys
 420 425 430
 Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro
 435 440 445
 Lys Tyr Gly Tyr Gln Gly Ser Trp Lys Leu
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 <211> 325
 <212> PRT
 <213> Chlamydia sp.
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 Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr
 35 40 45
 Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His Asp
 50 55 60
 Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser
 65 70 75 80
 Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe
 85 90 95
 Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn
 100 105 110
 His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Gln Gln Ala Leu
 115 120 125
 Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly
 130 135 140
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser
 145 150 155 160
 Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala Gly
 165 170 175
 Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg
 180 185 190
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr
 195 200 205
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His Leu Leu Asn
 210 215 220
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His
 225 230 235 240
 Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp Ala Tyr Arg
 245 250 255
 Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln Glu Thr Trp
 260 265 270
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val Val Arg Gly
 275 280 285
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly
 290 295 300
 Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr Gly Leu Ser Ala Gly
 305 310 315 320
 Ser Arg Val Arg Phe
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<400> 38
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<210> 39
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 <212> DNA
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<400> 39
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 <213> Chlamydia sp.

 <400> 42
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 <210> 43
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 <212> PRT
 <213> Chlamydia sp.

 <400> 43
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 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe
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 Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala
 35 40 45
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu
 50 55 60
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn
 65 70 75 80
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu
 85 90 95
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val
 100 105 110
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr
 115 120 125
 Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu
 130 135 140
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp
 145 150 155 160
 Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys
 165 170 175
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys
 180 185 190
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala
 195 200 205
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Ile Ala Ala Val
 210 215 220
 Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro
 225 230 235 240
 Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val
 245 250 255
 Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu
 260 265 270
 Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr
 275 280 285
 Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn
 290 295 300

Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala
 305 310 315 320
 Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val
 325 330 335
 Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala
 340 345 350
 Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn
 355 360 365
 Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu
 370 375 380
 Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys
 385 390 395 400
 Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser
 405 410 415
 Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg
 420 425 430
 Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala
 435 440 445
 Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn
 450 455 460
 Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser
 465 470 475 480
 Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg
 485 490 495
 Glu Lys Ala Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser
 500 505 510
 Leu Tyr Met Glu Ala Gly Ser Thr Trp Asp Phe Val Thr Pro Gln Pro
 515 520 525
 Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu
 530 535 540
 His Leu Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro
 545 550 555 560
 Pro Thr Asn Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser
 565 570 575
 Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe Glu Asp
 580 585 590
 Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln
 595 600 605
 Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys Pro Pro Ala Asn
 610 615 620
 Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr
 625 630 635 640
 Gln Gly Ser Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly
 645 650 655
 Pro Tyr Thr Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly
 660 665 670
 Pro Glu Arg Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile
 675 680 685
 Leu Asp Ile Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly
 690 695 700
 Arg Ser Tyr Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe
 705 710 715 720
 Tyr His Asp Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly
 725 730 735
 Gly Tyr Ser Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly
 740 745 750
 Leu Ala Phe Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys
 755 760 765
 Arg Ser Asn His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Gln
 770 775 780
 Gln Ala Leu Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala
 785 790 795 800

Ser Tyr Gly Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala
805 810 815
Glu Glu Ser Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile
820 825 830
Gly Ala Gly Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn
835 840 845
Glu Leu Arg Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu
850 855 860
Ser Phe Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His
865 870 875 880
Leu Leu Asn Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser
885 890 895
Ser Thr His Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp
900 905 910
Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln
915 920 925
Glu Thr Trp Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val
930 935 940
Val Arg Gly Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr
945 950 955 960
Gly His Gly Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr Gly Leu
965 970 975
Ser Ala Gly Ser Arg Val Arg Phe
980